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RAW SEQUENCE LISTING DATE: 09/05/2001
PATENT APPLICATION: **US/09/865,321** TIME: 19:13:28

Input Set : **A:\Peach571.app**
Output Set: **N:\CRF3\09052001\I865321.raw**

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 3 <110> APPLICANT: Peach, Robert J.
 4       Naemura, Joseph R
 5       Linsley, Peter S.
 6       Bajorath, Jurgen
 8 <120> TITLE OF INVENTION: SOLUBLE CTLA4 MUTANT MOLECULES AND USES THEREOF
10 <130> FILE REFERENCE: DB28NP/30436.57USU1
12 <140> CURRENT APPLICATION NUMBER: 09/865,321
13 <141> CURRENT FILING DATE: 2001-05-23
15 <150> PRIOR APPLICATION NUMBER: 60/287,576
16 <151> PRIOR FILING DATE: 2000-05-26
18 <150> PRIOR APPLICATION NUMBER: 60/214,065
19 <151> PRIOR FILING DATE: 2000-06-26
21 <160> NUMBER OF SEQ ID NOS: 8
23 <170> SOFTWARE: PatentIn Ver. 2.1
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26 <211> LENGTH: 41
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28 <213> ORGANISM: Artificial Sequence
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56 <220> FEATURE:
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62 ggcatcgcta gctttgtgtg tgagtatgca tctccaggca aatatactga ggtccgggtg 180
63 acagtgcttc ggcaggctga cagccaggtg actgaagtct gtgcggcaac ctacatgatg 240
64 gggaatgagt tgaccttcct agatgattcc atctgcacgg gcacctccag tggaaatcaa 300
65 gtgaacctca ctatccaagg actgagggcc atggacacgg gactctacat ctgcaaggtg 360
66 gagctcatgt acccaccgcc atactacgag ggcataggca acggaaccca gatttatgta 420
67 attgatccag aaccgtgccc agattctgat caggagccca aatcttctga caaaactcac 480
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68 acatccccac cgtccccagc acctgaactc ctgggggat cgtcagtctt cctcttcccc 540
69 ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg cgtggtggtg 600
70 gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg 660
71 cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc 720
72 gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg caaggtctcc 780
73 aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 840
74 gaaccacagg tgtacaccct gccccatcc cgggatgagc tgaccaagaa ccaggtcagc 900
75 ctgacctgcc tggtcaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 960
76 gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1020
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94 Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro
95 20 25 30
97 Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
98 35 40 45
100 Tyr Ala Ser Pro Gly Lys Tyr Thr Glu Val Arg Val Thr Val Leu Arg
101 50 55 60
103 Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
104 65 70 75 80
106 Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
107 85 90 95
109 Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp
110 100 105 110
112 Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr
113 115 120 125
115 Tyr Glu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
116 130 135 140
118 Pro Cys Pro Asp Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His
119 145 150 155 160
121 Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val
122 165 170 175
124 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
125 180 185 190
127 Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
128 195 200 205
130 Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
131 210 215 220
133 Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
134 225 230 235 240

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139 Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
140             260                 265                 270
142 Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
143         275                 280                 285
145 Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
146     290                 295                 300
148 Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
149 305                 310                 315                 320
151 Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
152                 325                 330                 335
154 Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
155             340                 345                 350
157 Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
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175 ggcatcgcta gctttgtgtg tgagtatgca tctccaggca aagccactga ggtccgggtg 180
176 acagtgcttc ggcaggctga cagccaggtg actgaagtct gtgcggcaac ctacatgatg 240
177 gggaatgagt tgaccttcct agatgattcc atctgcacgg gcacctccag tggaaatcaa 300
178 gtgaacctca ctatccaagg actgagggcc atggacacgg gactctacat ctgcaaggtg 360
179 gagctcatgt acccaccgcc atactacgag ggcataggca acggaaccca gatttatgta 420
180 attgatccag aaccgtgccc agattctgat caggagccca aatcttctga caaaactcac 480
181 acatccccac cgtccccagc acctgaactc ctgggggggat cgtcagtctt cctcttcccc 540
182 ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg cgtggtggtg 600
183 gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg 660
184 cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc 720
185 gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg caaggtctcc 780
186 aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 840
187 gaaccacagg tgtacaccct gcccccatcc cgggatgagc tgaccaagaa ccaggtcagc 900
188 ctgacctgcc tggtcaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 960
189 gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1020
190 ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 1080
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<220> FEATURE:
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            20                  25                  30
Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
        35                  40                  45
Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg
    50                  55                  60
Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
65                  70                  75                  80
Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
                85                  90                  95
Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp
            100                 105                 110
Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr
        115                 120                 125
Tyr Glu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
    130                 135                 140
Pro Cys Pro Asp Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His
145                 150                 155                 160
Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val
                165                 170                 175
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
            180                 185                 190
Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
        195                 200                 205
Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
    210                 215                 220
Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
225                 230                 235                 240
Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
                245                 250                 255
Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
            260                 265                 270
Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
        275                 280                 285
Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
    290                 295                 300
Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
305                 310                 315                 320
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
                325                 330                 335
Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
            340                 345                 350
Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
        355                 360                 365
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<223> OTHER INFORMATION: Description of Artificial Sequence:CTLA4Ig
<400> SEQUENCE: 7
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acagtgcttc ggcaggctga cagccaggtg actgaagtct gtgcggcaac ctacatgatg 240
gggaatgagt tgaccttcct agatgattcc atctgcacgg gcacctccag tggaaatcaa 300
gtgaacctca ctatccaagg actgagggcc atggacacgg gactctacat ctgcaaggtg 360
gagctcatgt acccaccgcc atactacctg ggcataggca acggaaccca gatttatgta 420
attgatccag aaccgtgccc agattctgat caggagccca aatcttctga caaaactcac 480
acatccccac cgtccccagc acctgaactc ctgggtggat cgtcagtctt cctcttcccc 540
ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg cgtggtggtg 600
gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg 660
cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg ggtggtcagc 720
gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg caaggtctcc 780
aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 840
gaaccacagg tgtacaccct gcccccatcc cgggatgagc tgaccaagaa ccaggtcagc 900
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  1               5                  10                  15
Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro
             20                  25                  30
Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
         35                  40                  45
Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg
     50                  55                  60
Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
 65                  70                  75                  80
Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
                 85                  90                  95
Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp
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